IFWO

RAW SEQUENCE LISTING DATE: 08/30/2004
PATENT APPLICATION: **US/10/660,194** TIME: 12:32:38

Input Set : **N:\Crf3\RULE60\10660194.raw**
Output Set: **N:\CRF4\08302004\J660194.raw**

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 1 <110> APPLICANT: FRANKEL, Fred R
 2         PORTNOY, Daniel A.
 3 <120> TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS COMPRISING LISTERIA DAL AND DAT GENES
 4 <130> FILE REFERENCE: 053893-5011-02
 5 <140> CURRENT APPLICATION NUMBER: US/10/660,194
 6 <141> CURRENT FILING DATE: 2003-09-11
 7 <150> PRIOR APPLICATION NUMBER: US/10/136,253
 8 <151> PRIOR FILING DATE: 2002-05-01
 9 <150> PRIOR APPLICATION NUMBER: 09/520,207
10 <151> PRIOR FILING DATE: 2000-03-07
11 <150> PRIOR APPLICATION NUMBER: PCT/US98/24357
12 <151> PRIOR FILING DATE: 1998-11-13
13 <150> PRIOR APPLICATION NUMBER: 08/972,902
14 <151> PRIOR FILING DATE: 1997-11-18
15 <160> NUMBER OF SEQ ID NOS: 9
16 <170> SOFTWARE: PatentIn version 3.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1107
20 <212> TYPE: DNA
21 <213> ORGANISM: Listeria monocytogenes
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24       aatataaaaa atgaacaaaa taaactcccg gaaagtgtcg acttatgggc agtagtcaaa       120
25       gctaatgcat atggtcacgg aattatcgaa gttgctagga cggcgaaaga agctggagca       180
26       aaaggtttct gcgtagccat tttagatgag gcactggctc ttagagaagc tggatttcaa       240
27       gatgacttta ttcttgtgct tggtgcaacc agaaaagaag atgctaatct ggcagccaaa       300
28       aaccacattt cacttactgt ttttagagaa gattggctag agaatctaac gctagaagca       360
29       acacttcgaa ttcatttaaa agtagatagc ggtatggggc gtctcggtat tcgtacgact       420
30       gaagaagcac ggcgaattga agcaaccagt actaatgatc accaattaca actggaaggt       480
31       atttacacgc attttgcaac agccgaccag ctagaaacta gttattttga caacaatta       540
32       gctaagttcc aaacgatttt aacgagttta aaaaacgac caacttatgt tcatacagcc       600
33       aattcagctg cttcattgtt acagccacaa atcgggtttg atgcgattcg ctttggtatt       660
34       tcgatgtatg gattaactcc ctccacagaa atcaaaacta gcttgccgtt tgagcttaaa       720
35       cctgcacttg cactctatac cgagatggtt catgtgaaag aacttgcacc aggcgatagc       780
36       gttagctacg gagcaactta tacagcaaca gagcgagaat gggttgcgac attaccaatt       840
37       ggctatgcgg atggattgat tcgtcattac agtggtttcc atgttttagt agacggtgaa       900
38       ccagctccaa tcattggtcg agtttgtatg gatcaaacca tcataaaact accacgtgaa       960
39       tttcaaactg gttcaaaagt aacgataatt ggcaaagatc atggtaacac ggtaacagca      1020
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41       cgcataccta gaaaatacat ccattag                                          1107
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 368
45 <212> TYPE: PRT
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51                     20                  25                 30
52         Val Asp Leu Trp Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly Ile
53                     35                  40                 45
54         Ile Glu Val Ala Arg Thr Ala Lys Glu Ala Gly Ala Lys Gly Phe Cys
55             50                  55                 60
56         Val Ala Ile Leu Asp Glu Ala Leu Ala Leu Arg Glu Ala Gly Phe Gln
57         65                  70                 75                     80
58         Asp Asp Phe Ile Leu Val Leu Gly Ala Thr Arg Lys Glu Asp Ala Asn
59                     85                  90                 95
60         Leu Ala Ala Lys Asn His Ile Ser Leu Thr Val Phe Arg Glu Asp Trp
61                     100                 105                110
62         Leu Glu Asn Leu Thr Leu Glu Ala Thr Leu Arg Ile His Leu Lys Val
63                     115                 120                125
64         Asp Ser Gly Met Gly Arg Leu Gly Ile Arg Thr Thr Glu Glu Ala Arg
65             130                 135                140
66         Arg Ile Glu Ala Thr Ser Thr Asn Asp His Gln Leu Gln Leu Glu Gly
67         145                 150                 155                    160
68         Ile Tyr Thr His Phe Ala Thr Ala Asp Gln Leu Glu Thr Ser Tyr Phe
69                         165                 170                175
70         Glu Gln Gln Leu Ala Lys Phe Gln Thr Ile Leu Thr Ser Leu Lys Lys
71                     180                 185                190
72         Arg Pro Thr Tyr Val His Thr Ala Asn Ser Ala Ala Ser Leu Leu Gln
73                     195                 200                205
74         Pro Gln Ile Gly Phe Asp Ala Ile Arg Phe Gly Ile Ser Met Tyr Gly
75             210                 215                220
76         Leu Thr Pro Ser Thr Glu Ile Lys Thr Ser Leu Pro Phe Glu Leu Lys
77         225                 230                 235                    240
78         Pro Ala Leu Ala Leu Tyr Thr Glu Met Val His Val Lys Glu Leu Ala
79                     245                 250                255
80         Pro Gly Asp Ser Val Ser Tyr Gly Ala Thr Tyr Thr Ala Thr Glu Arg
81                     260                 265                270
82         Glu Trp Val Ala Thr Leu Pro Ile Gly Tyr Ala Asp Gly Leu Ile Arg
83             275                 280                285
84         His Tyr Ser Gly Phe His Val Leu Val Asp Gly Glu Pro Ala Pro Ile
85             290                 295                300
86         Ile Gly Arg Val Cys Met Asp Gln Thr Ile Ile Lys Leu Pro Arg Glu
87         305                 310                 315                    320
88         Phe Gln Thr Gly Ser Lys Val Thr Ile Ile Gly Lys Asp His Gly Asn
89                     325                 330                335
90         Thr Val Thr Ala Asp Asp Ala Ala Gln Tyr Leu Asp Thr Ile Asn Tyr
91                     340                 345                350
92         Glu Val Thr Cys Leu Leu Asn Glu Arg Ile Pro Arg Lys Tyr Ile His
93                     355                 360                365
95  <210>  SEQ ID NO: 3
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96  <211> LENGTH: 386
97  <212> TYPE: PRT
98  <213> ORGANISM: Listeria monocytogenes
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103                  20                  25                  30
104      His Ile Met Ala Val Val Lys Ala Asn Ala Tyr Gly His Gly Asp Val
105              35                  40                  45
106      Gln Val Ala Arg Thr Ala Leu Glu Arg Gly Pro Pro Pro Ala Val Ala
107          50                  55                  60
108      Phe Leu Asp Glu Ala Leu Ala Leu Arg Glu Lys Gly Ile Glu Ala Pro
109      65                  70                  75                  80
110      Ile Leu Val Leu Gly Ala Ser Arg Pro Ala Asp Ala Ala Leu Ala Ala
111                  85                  90                  95
112      Gln Gln Arg Ile Ala Leu Thr Val Phe Arg Ser Asp Trp Leu Glu Glu
113                  100                 105                 110
114      Ala Ser Ala Leu Tyr Ser Gly Pro Phe Pro Ile His Phe His Leu Lys
115              115                 120                 125
116      Met Asp Thr Gly Met Gly Arg Leu Gly Val Lys Asp Glu Glu Glu Thr
117          130                 135                 140
118      Lys Arg Ile Val Ala Leu Ile Glu Arg His Pro His Phe Val Leu Glu
119      145                 150                 155                 160
120      Gly Leu Tyr Thr His Phe Ala Thr Ala Asp Glu Val Asn Thr Asp Tyr
121                  165                 170                 175
122      Phe Ser Tyr Gln Tyr Thr Arg Phe Leu His Met Leu Glu Trp Leu Pro
123              180                 185                 190
124      Ser Arg Pro Pro Leu Val His Cys Ala Asn Ser Ala Ala Ser Leu Arg
125              195                 200                 205
126      Phe Pro Asp Arg Thr Phe Asn Met Val Arg Phe Gly Ile Ala Met Tyr
127          210                 215                 220
128      Gly Leu Ala Pro Ser Pro Gly Ile Lys Pro Leu Leu Pro Tyr Pro Leu
129      225                 230                 235                 240
130      Lys Glu Ala Phe Ser Leu His Ser Arg Leu Val His Val Lys Lys Leu
131                  245                 250                 255
132      Gln Pro Gly Glu Lys Val Ser Tyr Gly Ala Thr Tyr Thr Ala Gln Thr
133                  260                 265                 270
134      Glu Glu Trp Ile Gly Thr Ile Pro Ile Gly Tyr Ala Asp Gly Val Arg
135              275                 280                 285
136      Arg Leu Gln His Phe His Val Leu Val Asp Gly Gln Lys Ala Pro Ile
137          290                 295                 300
138      Val Gly Arg Ile Cys Met Asp Gln Cys Met Ile Arg Leu Pro Gly Pro
139      305                 310                 315                 320
140      Leu Pro Val Gly Thr Lys Val Thr Leu Ile Gly Arg Gln Gly Asp Glu
141                  325                 330                 335
142      Val Ile Ser Ile Asp Asp Val Ala Arg His Leu Glu Thr Ile Asn Tyr
143              340                 345                 350
144      Glu Val Pro Cys Thr Ile Ser Tyr Arg Val Pro Arg Ile Phe Phe Arg
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148       Ser Ala
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153 <212> TYPE: PRT
154 <213> ORGANISM: Listeria monocytogenes
155 <400> SEQUENCE: 4
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158       Ser Ala Ile Lys Glu Asn Val Ser Asn Met Lys Lys His Ile Gly Glu
159                      20                  25                  30
160       His Val His Leu Met Ala Val Glu Lys Ala Asn Ala Tyr Gly His Gly
161          35                  40                  45
162       Asp Ala Glu Thr Ala Lys Ala Ala Leu Asp Ala Gly Ala Ser Cys Leu
163          50                  55                  60
164       Ala Met Ala Ile Leu Asp Glu Ala Ile Ser Leu Arg Lys Lys Gly Leu
165       65                  70                  75                  80
166       Lys Ala Pro Ile Leu Val Leu Gly Ala Val Pro Pro Glu Tyr Val Ala
167                      85                  90                  95
168       Ile Ala Ala Glu Tyr Asp Val Thr Leu Thr Gly Tyr Ser Val Glu Trp
169                      100                 105                 110
170       Leu Gln Glu Ala Ala Arg His Thr Lys Lys Gly Ser Leu His Phe His
171          115                 120                 125
172       Leu Lys Val Asp Thr Gly Met Asn Arg Leu Gly Val Lys Thr Glu Glu
173          130                 135                 140
174       Glu Val Gln Asn Val Met Ala Ile Leu Asp Arg Asn Pro Arg Leu Lys
175       145                 150                 155                 160
176       Cys Lys Gly Val Phe Thr His Phe Ala Thr Ala Asp Glu Lys Glu Arg
177                      165                 170                 175
178       Gly Tyr Phe Leu Met Gln Phe Glu Arg Phe Lys Glu Leu Ile Ala Pro
179                      180                 185                 190
180       Leu Pro Leu Lys Asn Leu Met Val His Cys Ala Asn Ser Ala Ala Gly
181          195                 200                 205
182       Leu Arg Leu Lys Lys Gly Phe Phe Asn Ala Val Arg Phe Gly Ile Gly
183          210                 215                 220
184       Met Tyr Gly Leu Arg Pro Ser Ala Asp Met Ser Asp Glu Ile Pro Phe
185       225                 230                 235                 240
186       Gln Leu Arg Pro Ala Phe Thr Leu His Ser Thr Leu Ser His Val Lys
187                      245                 250                 255
188       Leu Ile Arg Lys Gly Glu Ser Val Ser Tyr Gly Ala Glu Tyr Thr Ala
189                      260                 265                 270
190       Glu Lys Asp Thr Trp Ile Gly Thr Val Pro Val Gly Tyr Ala Asp Gly
191          275                 280                 285
192       Trp Leu Arg Lys Leu Lys Gly Thr Asp Ile Leu Val Lys Gly Lys Arg
193          290                 295                 300
194       Leu Lys Ile Ala Gly Arg Ile Cys Met Asp Gln Phe Met Val Glu Leu
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195          305                    310                    315                    320
196          Asp Gln Glu Tyr Pro Pro Gly Thr Lys Val Thr Leu Ile Gly Arg Gln
197                          325                    330                    335
198          Gly Asp Glu Tyr Ile Ser Met Asp Glu Ile Ala Gly Arg Leu Glu Thr
199                          340                    345                    350
200          Ile Asn Tyr Glu Val Ala Cys Thr Ile Ser Ser Arg Val Pro Arg Met
201                          355                    360                    365
202          Phe Leu Glu Asn Gly Ser Ile Met Glu Val Arg Asn Pro Leu Leu Gln
203                  370                    375                    380
204          Val Asn Ile Ser Asn
205                  385
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208   <211>  LENGTH: 870
209   <212>  TYPE: DNA
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211   <400>  SEQUENCE: 5
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214          ttctttactt ataatgaaca cattgatcgc ttatatgcta gtgcagcaaa aattgactta    180
215          gttattcctt attccaaaga agagctacgt gaattacttg aaaaattagt tgccgaaaat    240
216          aatatcaata cagggaatgt ctatttacaa gtgactcgtg gtgttcaaaa cccacgtaat    300
217          catgtaatcc ctgatgattt ccctctagaa ggcgttttaa cagcagcagc tcgtgaagta    360
218          cctagaaacg agcgtcaatt cgttgaaggt ggaacggcga ttacagaaga agatgtgcgc    420
219          tggttacgct gtgatattaa gagcttaaac cttttaggaa atattctagc aaaaaataaa    480
220          gcacatcaac aaaatgcttt ggaagctatt ttacatcgcg gggaacaagt aacagaatgt    540
221          tctgcttcaa acgtttctat tattaaagat ggtgtattat ggacgcatgc ggcagataac    600
222          ttaatcttaa atggtatcac tcgtcaagtt atcattgatg ttgcgaaaaa gaatggcatt    660
223          cctgttaaag aagcggattt cactttaaca gaccttcgtg aagcggatga agtgttcatt    720
224          tcaagtacaa ctattgaaat tacacctatt acgcatattg acggagttca agtagctgac    780
225          ggaaaacgtg gaccaattac agcgcaactt catcaatatt ttgtagaaga aatcactcgt    840
226          gcatgtggcg aattagagtt tgcaaaataa                                     870
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229   <211>  LENGTH: 289
230   <212>  TYPE: PRT
231   <213>  ORGANISM: Listeria monocytogenes
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234          1               5                   10                  15
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236                          20                  25                  30
237          Val Val Arg Leu Tyr Asn Gly Lys Phe Phe Thr Tyr Asn Glu His Ile
238                  35                  40                  45
239          Asp Arg Leu Tyr Ala Ser Ala Ala Lys Ile Asp Leu Val Ile Pro Tyr
240                  50                  55                  60
241          Ser Lys Glu Glu Leu Arg Glu Leu Leu Glu Lys Leu Val Ala Glu Asn
242          65                  70                  75                  80
243          Asn Ile Asn Thr Gly Asn Val Tyr Leu Gln Val Thr Arg Gly Val Gln
244                          85                  90                  95
245          Asn Pro Arg Asn His Val Ile Pro Asp Asp Phe Pro Leu Glu Gly Val
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Seq#:1; Line(s) 3

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